



Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon Number	Exon length (bp)	cDNA position	splice acceptor	flanking exon sequence	splice donor	Intron number	Intron Size approximate (Kb)
1	55	1-55		...CTG CAC G L H	GTAAGGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCC.....GAC GTG V S D V	GTGAGTCCCG	2	Unknown
3	45	196-240	TTTTTTTGAAG	GAT GAG.....CAA ATG D E Q M	GTAAGTTAAG	3	9.0
4	110	241-350	TGTGTGTCAG	TCT TGG.....AAC AG S W N S	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG	T GCT GAT.....CCT CCA G A D P P	GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	GC ATA.....CTA GTG G G I L V	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	GA ATC.....TCC CTG G G I S L	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	GG ATA.....TTG ATA G G I L I	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAG.....AAG TGG A Q K W	GTACGTTCTT	9	5.0
10	519	991-1509	GTCTCCCCAG	ACC AGA... T R			

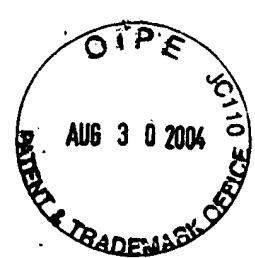
FIG. 1

Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

DNA	EXONS CONT.	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335	L76630
CHR15 HYBRID	5-10 1-10	+TG -TG	C/T	G/A	C/C	C/C	6GT 8GT
YAC							
D-948a10	5-10	-TG	T	A	C	C	6GT
D-853b12	6-10	-TG	T	A	C	C	6GT
D/F 969b11	5-10 1-10	+TG -TG	C/T	G/A	C/T	C/C	6GT 8GT
F-134h10	1-10	+TG	C	G	C	C	8GT
F-776a12	1-10	+TG	C	G	C	C	8GT
F-791e6	1-10	+TG	C	G	C	C	8GT
F-811b6	1-10	+TG	C	G	C	C	8GT
F-953g6	1-10	+TG	C	G	C	C	8GT
F-859c11	1-10	+TG	C	G	C	C	8GT
F-810f11	1-10	+TG	C	G	C	C	8GT
F-801e1	1-10	+TG	C	G	C	C	8GT
BAC							
F-467o18	1-10	+TG	C	G	C	T	8GT

FIG. 2

DNA	Control #	EXON 6 +/- 497-498	EXON 7 654	EXON 7 690	EXON 10 1269	EXON 10 1335
Control Genomic DNA	43	+/+ 10 +/- 33 -/- 0	C/C 5 C/T 38 T/T 0	G/G 0 G/A 43 A/A 0	C/C 6 C/T 36 T/T 1	C/C 24 C/T 19 T/T 0





# Expression Analysis of Sequence Variants

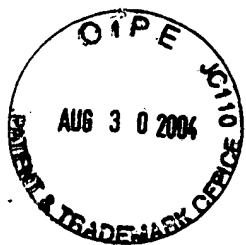
Subj	Bases 497-498			Base 654			Base 690			Base 933			Base 1296			Base 1335		
	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA	DNA	1-10 cDNA	5-10 cDNA
SL061	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	C	C	C
SL084	+	+	+	C	C	C	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL111	+/-	+	+/-	CT	C	CT	GA	G	GA	G	G	G	CT	CT	CT	CT	CT	CT
SL097	+	+	+	CT	C	CT	GA	G	GA	G	G	G	CT	C	CT	C	C	C
SL089	+	+	+	C	C	C	GA	GA	GA	GA	GA	GA	CT	CT	CT	C	C	C
SHSY	+/-	+	+/-	CT	C	CT	GA	GA	GA	GA	GA	GA	C	C	C	C	C	C

FIG. 3

-392 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg aggccgagag  
 AP-2  
 -322 ccgcctcggt ggagactggg ggtggagggt ccgggagcgt acccagcgcc gggagtacct cccgctcaca  
 -252 cctcgggctg cagttccctg ggtggccgcc gagacgctgg cccgggctgg agggatggcg gggcgggggac  
 -182 gggggcgggg gcggggctcg tcacgtggag aggcgcgcgg gggcgggcgg gcgcgccggc  
 CREB Sp1  
 -112 tccttaagg cgcgcgagcc ggcggcgag gtgccttgt ggccgcaggc gcaggcccg gcgacagcg  
 -42 agacgtggag cgcgccggct cgtgcagct ccgggactca acATGCGCTG CTCGCCCGGA GCGCTCTGCG  
 Met  
 +29 TGGCGCTGGC CCGTCCCTC CTGCACGGta aagccac

**FIG. 4**





<b>EXON D</b> 297bp	1 CAGGCCGCCA CACGGCGGCG AGCGGCTCGG TTCAAGGCCA CCCACCGCAA	CATAGCTCCC GGGAGAGGTG GACTGGCTCC AACCGAAGTT CATTAAGgtg 297	GCCAAGTCCT GAGCCGCGAG TTTTCCGCGC ACTGGCCTCT agtgcgc.....	CGGTGCCCCCT AGCTCGGCGG CCCTCCCCGCC ATCTTCCAGG agtcgcgc.....	TGCCATTTTTC GGGGCCCCCG GGAGGTGAGG AGAACCAGGA agtcgcgc.....	CAGCCGCGGTC CTGGTGGCCG GGAAGATGTC GCCACAGCCG agtcgcgc.....	CCACGAGGGT CGGCCATGAC CATGTCAGGG CGGCTCACGC agtcgcgc.....
<b>EXON C</b> 125bp	.....ctc TATCTACACG AAgtgagttg 422	atttcagATT ACTCAGATCT ta..... 422	ACAAGTGGAC TGTGTGCACC ta..... 422	ACCTGAGTCA CCCATTATTG ta..... 422	GCAGGACCTG ACAATCCAAA ta..... 422	GAATCCCAGA GGTGCAGAAA ta..... 422	TGAGAGAGCT GCACTCTGAC ta..... 422
<b>EXON B</b> 64bp	...ttaaccac TTTCAGgtag 486	agATAATGAA gateat..... 486	ACAACCACCA gateat..... 486	TCGGTTAAAT gateat..... 486	TTGATGCAAA gateat..... 486	AATATTGCAT gateat..... 486	CTACCAGCAT gateat..... 486
<b>EXON A</b> 47bp	.....ttta aca..... 487	ttctagTTCC gateat..... 487	AATTGCTAAT gateat..... 487	CCAGCATTTC gateat..... 487	TGGATAGCTG gateat..... 487	CAAACGCGA gateat..... 487	TATgtaagta 533
<b>EXON 5</b> 80bp	....ctgtttc GCAATTGCCAG 534	tagTGCTGAT GCAATTGCCAG 534	GAGCGCTTTG TACCTGCCTC 534	ACGCCACATT CAGgtaagctgca..... 613	CCACACTAAC CAGgtaagctgca..... 613	GTGTGTGGTGA gateat..... 613	ATTCTTCTGG gateat..... 613
<b>EXON 6</b> 27bp	....accacaca cagGCATATT 614	cagGCATATT gateat..... 614	CAAGAGTTCC gateat..... 614	TGCTACATCG gateat..... 614	gateat..... 614	gateat..... 614	gateat..... 614

FIG. 6

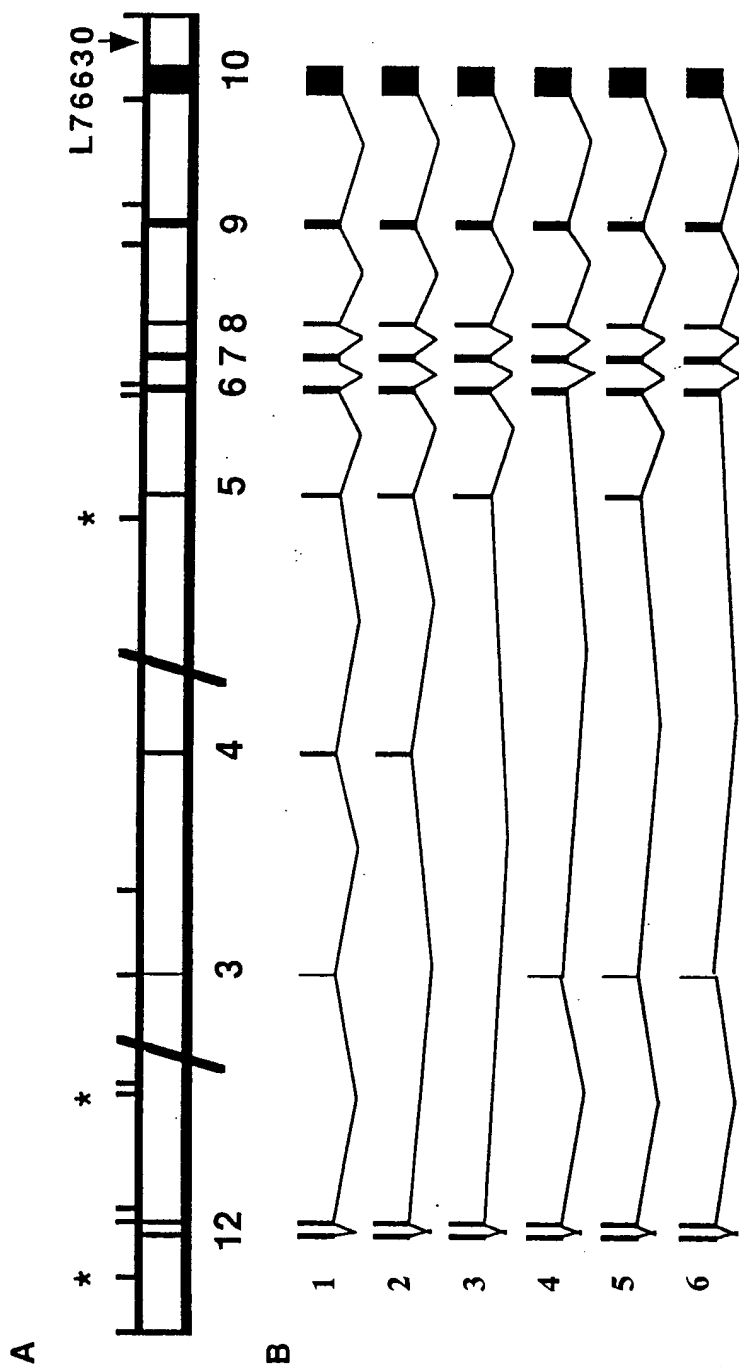


FIG. 7



1 agaacgcaag ggagaggtag agcctggcct tgggcagccc ctggcctggc cagaggcgcg  
61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc  
121 gggagtacct cccgctcaca cctcgggctg cagttccctg ggtggccgcc gagacgctgg  
181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag  
241 aggcgcgcgg gggcggggcg ggcggggggc cgcgcccggc tccttaaagg cgcgcgagcc  
301 gagcggcgag gtgcctctgt ggccgcaggc gcaggcccgg gcgacagccg agacgtggag  
361 cgcgccggct cgctgcagct cggggactca ac

FIG. 8

1 caggccgcca catagctccc gccaaagtcc cggtgcccct tgccattttc cagccgcgct  
61 cccacgaggg tcacggcgcc ggggagaggt ggagccgcga gagctcggcc gggggccccc  
121 cctgggtggc gcggccatga cagcggctcg ggactggctc cttttccgcg cccctcccgc  
181 cggaggtgag gggaagatgt ccatgtcagg gttcaaggcc aaaccgaagt tactggcctc  
241 tatcttccag gagaaccagg agccacagcc gcggctcacg ccccaccgca acattaagat  
301 tacaagtgga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac  
361 gactcagatc ttgttggtcac cccattatt gacaatccaa aggtgcagaa agcactctga  
421 caaataatga aacaaccacc atcgggttaa tttgatgcaa aaatattgca tctaccagca  
481 ttttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga  
541 tgagcgcttt gacgccacat tccacactaa cgtgttggtg aattcttctg ggcattgcca  
601 gtacctgcct ccaggcatat tcaagagttc ctgctacatc g

FIG. 9

1 agccctttcc caggcggtag cgggggcagt ggtgctgttg cccttttaaa ctgcggcttg  
61 acgggagccg cgcctcctgt cgggtggagtc ggttataaaag ggagcagccc cgcaggccgc  
121 cacatagctc ccgccaagtc ctcggtgccc cttgccattt tccagccgcg ctcccacgag  
181 ggtcacggcg gcggggagag gtggagccgc gagagctcgg ccggggggccc cgcctgggtg  
241 ccgcggccat gacagcggct cgggactggc tccttttccg cgccccctcc gccggaggtg  
301 aggggaagat gtccatgtca gggttcaagg ccaaaccgaa gttactggcc tctatcttcc  
361 aggagaacca ggagccacag ccgcggctca cgccccaccg caacattaag attacaagtg  
421 gacacctgag tcagcaggac ctggaatccc agatgagaga gcttatctac acgactcaga  
481 tcttggtgtc accccatta ttgacaatcc aaaggtgcag aaagcactct gacaattcca  
541 attgctaadc cagcatttgt ggatagctgc aaactgcgat attgctgatg agcgctttga  
601 cgccacattc cacactaacg tgttggtgaa ttcttctggg cattgccagt acctgcctcc  
661 aggcataattc aagagttcct gctacatcg

FIG. 10